

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/555,407  
Source: PCT  
Date Processed by STIC: 11/15/2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 11/15/2005

PATENT APPLICATION: US/10/555,407

TIME: 10:09:47

Input Set : A:\SeqListing.txt

Output Set: N:\CRF4\11152005\J555407.raw

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3 <110> APPLICANT: Dale L. Ludwig
5 <120> TITLE OF INVENTION: Fully Human Antibodies Directed Against the Human Insulin-
Like
6      Growth Factor-1 Receptor
8 <130> FILE REFERENCE: 11245/53202
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/555,407
C--> 11 <141> CURRENT FILING DATE: 2005-11-01
13 <150> PRIOR APPLICATION NUMBER: PCT/US2004/013852
14 <151> PRIOR FILING DATE: 2004-05-03
16 <150> PRIOR APPLICATION NUMBER: US 60/467,177
17 <151> PRIOR FILING DATE: 2003-05-01
19 <160> NUMBER OF SEQ ID NOS: 33
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 390
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(390)
33 <400> SEQUENCE: 1
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35 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
36 1          5          10          15
38 tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat      96
39 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
40          20          25          30
42 gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg      144
43 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
44          35          40          45
46 gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc      192
47 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
48          50          55          60
50 cag ggc aga gtc acg att acc gcg gac aaa tcc acg agc aca gcc tac      240
51 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
52 65          70          75          80
54 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt      288
55 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
56          85          90          95
58 gcg aga gcg cca tta cga ttt ttg gag tgg tcc acc caa gac cac tac      336
59 Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln Asp His Tyr
60          100          105          110
62 tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc      384
63 Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val

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66 tca agc
67 Ser Ser
68      130
71 <210> SEQ ID NO: 2
72 <211> LENGTH: 130
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 2
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79 1          5          10          15
82 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
83          20          25          30
86 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
87          35          40          45
90 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
91          50          55          60
94 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
95 65          70          75          80
98 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
99          85          90          95
102 Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln Asp His Tyr
103          100          105          110
106 Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
107          115          120          125
110 Ser Ser
111      130
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 1440
116 <212> TYPE: DNA
117 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
121 <221> NAME/KEY: CDS
122 <222> LOCATION: (1)..(1440)
124 <400> SEQUENCE: 3
125 atg gga tgg tca tgt atc atc ctt ttt cta gta gca act gca act gga      48
126 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
127 1          5          10          15
129 gta cat tca gag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag      96
130 Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
131          20          25          30
133 cct ggg tcc tgc gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc      144
134 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
135          35          40          45
137 agc agc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt      192
138 Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
139          50          55          60
141 gag tgg atg gga ggg atc atc cct atc ttt ggt aca gca aac tac gca      240
142 Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala

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143	65		70		75		80	
145	cag aag ttc cag ggc aga gtc acg att acc gcg gac aaa tcc acg agc	288						
146	Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser							
147			85		90		95	
149	aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336						
150	Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val							
151			100		105		110	
153	tat tac tgt gcg aga gcg cca tta cga ttt ttg gag tgg tcc acc caa	384						
154	Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln							
155			115		120		125	
157	gac cac tac tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg	432						
158	Asp His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr							
159			130		135		140	
161	gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg	480						
162	Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu							
163	145		150		155		160	
165	gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc	528						
166	Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys							
167			165		170		175	
169	ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca	576						
170	Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser							
171			180		185		190	
173	ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc	624						
174	Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser							
175			195		200		205	
177	tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc	672						
178	Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser							
179			210		215		220	
181	ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac	720						
182	Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn							
183	225		230		235		240	
185	acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac	768						
186	Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His							
187			245		250		255	
189	aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc	816						
190	Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val							
191			260		265		270	
193	ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc	864						
194	Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr							
195			275		280		285	
197	cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag	912						
198	Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu							
199			290		295		300	
201	gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag	960						
202	Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys							
203	305		310		315		320	
205	aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc	1008						
206	Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser							
207			325		330		335	

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209 gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag      1056
210 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
211          340          345          350
213 tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc      1104
214 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
215          355          360          365
217 tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc      1152
218 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
219          370          375          380
221 cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg      1200
222 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
223 385          390          395          400
225 gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat      1248
226 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
227          405          410          415
229 ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc      1296
230 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
231          420          425          430
233 gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gag aag agc agg      1344
234 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
235          435          440          445
237 tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg      1392
238 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
239          450          455          460
241 cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga      1440
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243 465          470          475
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 479
248 <212> TYPE: PRT
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 4
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254 1          5          10          15
257 Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
258          20          25          30
261 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
262          35          40          45
265 Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
266          50          55          60
269 Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
270 65          70          75          80
273 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
274          85          90          95
277 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
278          100          105          110
281 Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln
282          115          120          125
285 Asp His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr

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286      130      135      140
289 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
290 145      150      155      160
293 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
294      165      170      175
297 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
298      180      185      190
301 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
302      195      200      205
305 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
306      210      215      220
309 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
310 225      230      235      240
313 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
314      245      250      255
317 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
318      260      265      270
321 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
322      275      280      285
325 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
326      290      295      300
329 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
330 305      310      315      320
333 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
334      325      330      335
337 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
338      340      345      350
341 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
342      355      360      365
345 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
346      370      375      380
349 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
350 385      390      395      400
353 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
354      405      410      415
357 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
358      420      425      430
361 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
362      435      440      445
365 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
366      450      455      460
369 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 465      470      475
373 <210> SEQ ID NO: 5
374 <211> LENGTH: 327
375 <212> TYPE: DNA
376 <213> ORGANISM: Homo sapiens
379 <220> FEATURE:
380 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 11/15/2005  
PATENT APPLICATION:    US/10/555,407      TIME: 10:09:48

Input Set : A:\SeqListing.txt  
Output Set: N:\CRF4\11152005\J555407.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:31,32,33

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/555,407

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Input Set : A:\SeqListing.txt

Output Set: N:\CRF4\11152005\J555407.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date